Agro-morphological characterization and assessment of variability, heritability, genetic advance and divergence in bacterial blight resistant rice genotypes

ABSTRACT

Genetic based knowledge of different growth traits including morphological, physiological and developmental plays fundamental role in the improvement of rice. Genetic divergence allows superior recombinants which are essential in any crop development project. Forty-one rice genotypes including bacterial blight (BB) resistant and susceptible checks were assessed for 13 morphological traits. Among the genotypes, almost all the traits exhibited highly significant variation. The higher extent of genotypic (GCV) as well as phenotypic coefficients of variation (PCV) were noticed for number of tillers hillī 1, total number of spikelets panicleī 1, number of filled grains panicleī 1, and yield hillī 1. High heritability together with high genetic advance was observed for total number of spikelets panicleī 1, number of filled grains panicleī 1, and yield hillī 1 indicating dominant role of additive gene action in the expression of these traits. Number of filled grains panicleī 1 exhibited positive correlation with most of the traits. Yield hillī 1 showed a good number of highly significant positive correlations with number of filled grain panicleī 1, total number of spikelets panicleī 1, 1000 grain weight hillī 1, number of panicle hillī 1, and panicle length. The UPGMA dendrogram divided all the genotypes in to six major clusters. The PCA showed 13 morphological traits generated about 71% of total variation among all the genotypes under this study. On the basis of 13 morphological traits, genotypes such as IRBB2, IRBB4, IRBB13, IRBB21, and MR263 could be hybridized with genotypes MR84, MR159, MRQ50, MRQ74, PH9 and IR8 in order to develop suitable BB resistant rice genotypes.

Keyword: Genetic diversity; Heritability; Bacterial blight resistant rice genotypes; Cluster analysis; Principal component analysis